

1 GCGGCAGCGG CGGCGGCTGA GGAGGGCCCCG GCCTGCGAGA GCCTCAGTGG
 51 GAGCCGGGCTC AGCCCTCGGC CACCATGTCTG GCGCCGTCGG AGGAGGAGGA
 101 GTACGCGCGG CTGGTGATGG AGGCGCAGCC GGAGTGGCTG CGCGTCGAGG
 151 TGAAGCGGCT GTCCACGAG CTGGCCGAGA CCACGCGTGA GAAGATCCAG
 201 GCGGCCGAGT ACGGGCTGGC GGTGCTCGAG GAGAAGCACC AGCTCAAGCT
 251 GCAGTTCGAG GAGCTCGAGG TGGACTATGA GGCTATCCGC AGCGAGATGG
 301 AGCAGCTCAA GGAGGCCTTT GGACAAGCAC ACACAAACCA CAAGAAGGTG
 351 GCTGCTGACG GAGAGAGCCG GGAGGAGAGC CTGATCCAGG AGTCGGCCTC
 401 CAAGGAGCAG TACTACGTGC GGAAGGTGCT AGAGCTGCAG ACGGAGCTGA
 451 AGCAGTTGCG CAATGTCCTC ACCAACACGC AGTCGGAGAA TGAGCGCCTG
 501 GCCTCTGTGG CCCAGGAGCT GAAGGAGATC AACCAGAATG TGGAGATCCA
 551 GCGTGGCCGC CTGCGGGATG ACATCAAGGA GTACAAATTC CGGGAAGCTC
 601 GTCTGCTGCA GGACTACTCG GAACTGGAGG AGGAGAACAT CAGCCTGCAG
 651 AAGCAAGTGT CTGTGCTCAG ACAGAACCAG GTGGAGTTTG AGGGCCTCAA
 701 GCATGAGATC AAGCGTCTGG AGGAGGAGAC CGAGTACCTC AACAGCCAGC
 751 TGGAGGATGC CATCCGCCTC AAGGAGATCT CAGAGCGGCA GCTGGAGGAG
 801 GCGCTGGAGA CCCTGAAGAC GGAGCGCGAA CAGAAGAACA GCCTGCGCAA
 851 GGAGCTGTCA CACTACATGA GCATCAATGA CTCCTTCTAC ACCAGCCACC
 901 TGCATGTCTC GCTGGATGGC CTCAAGTTCA GTGACGATGC TGCCGAGCCC
 951 AACAAACGATG CCGAGGCCCT GGTCAATGGC TTTGAGCACG GCGGCCTGGC
 1001 CAAGCTGCCA CTGGACAACA AGACCTCCAC GCCCAAGAAG GAGGGCCTCG
 1051 CACCGCCCTC CCCCAGCCTC GTCTCCGACC TACTCAGTGA GCTCAACATC
 1101 TCTGAGATCC AGAAGCTGAA GCAGCAGCTG ATGCAGATGG AGCGGGAAAA
 1151 GCGGGGCTG CTGGCAACGC TGCAGGACAC ACAGAAGCAG CTGGAGCACA
 1201 CGCGGGGCTC CCTGTCAGAA CAGCAGGAGA AGGTGACCCG CCTCACAGAG
 1251 AATCTGAGTG CCCTGCGGCG CCTGCAGGCC AGCAAGGAGC GGCAGACAGC
 1301 CCTGGACAAC GAGAAGGACC GTGACAGCCA TGAGGATGGG GACTACTACG
 1351 AGGTGGACAT CAACGGGCCT GAGATCTTGG CCTGCAAGTA CCATGTGGCT
 1401 GTGGCTGAGG CTGGCGAGCT CCGCGAGCAG CTCAAGGCAC TGCGCAGCAC
 1451 GCACGAGGCT CGTGAGGCCC AGCACGCCGA GGAGAAGGGC CGCTATGAGG
 1501 CTGAGGGCCA GGCATCAGC GAGAAGGTCT CCCTGCTAGA GAAGGCCAGC

FIGURE 1

1551	CGCCAGGACC	GCGAGCTGCT	GGCCCGGCTG	GAGAAGGAGC	TAAAGAAGGT
1601	GAGCGACGTC	GCCGGCGAGA	CACAGGGCAG	CCTGAGTGTG	GCCCAGGATG
1651	AGCTGGTGAC	CTTCAGTGAG	GAGCTGGCCA	ATCTCTACCA	CCACGTGTGC
1701	ATGTGCAACA	ATGAGACACC	CAACCGTGTC	ATGCTGGACT	ACTACCGCGA
1751	GGGCCAGGGC	GGGGCCGGCC	GCACCAGTCC	CGGGGGCCGC	ACCAGCCCCG
1801	AGGCGCGTGG	CCGGCGCTCA	CCCATCCTCC	TACCCAAGGG	GCTGCTGGCT
1851	CCTGAGGCGG	GCCGAGCAGA	TGGTGGGACG	GGGGACAGCA	GCCCCTCGCC
1901	TGGCTCCTCA	CTGCCATCAC	CCCTGAGTGA	CCCACGCCGG	GAGCCCATGA
1951	ACATCTACAA	CCTGATCGCT	ATCATCCGTG	ACCAGATCAA	GCACCTGCAG
2001	GCAGCCGTGG	ACCGCACCAC	GGAGCTGTCA	CGCCAGCGCA	TTGCCTCTCA
2051	GGAGCTGGGC	CCCGCCGTGG	ACAAGGACAA	GGAAGCGCTT	ATGGAGGAGA
2101	TCCTCAAGCT	GAAGTCGCTG	CTCAGCACCA	AGCGGGAGCA	GATCACCACG
2151	CTGCGCACTG	TGCTCAAGGC	CAACAAGCAG	ACGGCCGAGG	TGGCCCTTGC
2201	CAACCTGAAG	AGCAAGTATG	AGAATGAGAA	GGCCATGGTT	ACCGAGACCA
2251	TGATGAAGCT	GCGCAATGAG	CTCAAGGCCC	TCAAGGAGGA	CGCAGCCACC
2301	TTCTCCTCGC	TGCGTGCTAT	GTTTGCCACC	AGGTGTGACG	AGTACATTAC
2351	ACAGCTGGAT	GAGATGCAGC	GGCAGCTGGC	GGCTGCTGAG	GACGAGAAGA
2401	AGACGCTGAA	CTCGTGCTG	CGCATGGCCA	TCCAGCAGAA	GCTGGCGCTG
2451	ACCCAGCGGC	TGGAGCTGCT	CGAGCTGGAC	CATGAGCAGA	CCCGGCGTGG
2501	CCGTGCCAAA	GCCGCCCCGA	AGACCAAGCC	AGCCACACCG	AGCCTGTAGA
2551	GTAGCTGCCA	GGAGGACTTG	GCCACCCGGC	CCTGTCACAC	TGCAGCCCCT
2601	TCCCTTCC	TCTCGTGGCC	CACAAGGAGG	AAGGAAGGGC	AACCTAAAAG
2651	CCCACTTAGA	AACTTTTGG	ATATGCCACT	GCAATTCTTT	TCAAAATAGC
2701	ATTCCCCAGG	TTTTTAAATGG	GAGGAAAAAA	AGCTTTAATG	TTGAGCATGC
2751	TGCGAGCTGC	TGCGTGGA	GGCCTCTGTA	TGGGCCGAAG	ACCCTTCTTC
2801	CCTGGCTGCC	AGGCTCGCCA	GGAGCCCACT	GGAAACGCCC	ACCACGGGGG
2851	CTCCTTGTTA	CACATGTTCT	TTTTTTATCC	GATCAACCTG	TGCACTTTTG
2901	ATATTTTGAT	ATTATATTTG	CTTCCTTAAT	TCCTCGCGTA	GAGACGGTCT
2951	CAGGTGCCGT	GGTCTATGCT	CGTGGTCCTG	TAGCTGTCCG	CCTCAGCTCC
3001	CACCGTGTTT	GTCTGGTGTC	AGCACGAGGC	AGAGCTGTGT	GCTCCATAGC
3051	GTGTAGCTTT	AGACTCGGAG	ATGAGTGCTT	TGACCCAGCG	AGGAGCTCAG
3101	CTAAGTGTAT	CCACGCTGTG	GTTCAGCAGC	CTTTAGATCA	TACGGCATTG
3151	TGGTTCATGT	TTGAAATTAC	AGATTTTAAA	TGCCATGTTT	ATTAAGAAAT

3201 CCAGGGTATT CAGATTCTGG GGTTTTTCAT ATTGTATTAT TATTATTCTT
3251 AGGAATAGTT CAATGTAACA AGAAGAAAAC TTGACCTTTG CTCTGGTTAA
3301 AACAGTAATA GGCACCTGAA AAAAAAAGAT AAATTATTGA ATGAGTAGTA
3351 TTACCTACAA ATTCCAGAAT TTTCTGGGTT TTAGGACGTT GTGAAGCATG
3401 ACTGATTAAC AGAATTTTAT ACAACTGTAC CAATAAAATT CCAAATTGGA
3451 ATTGTTTTGT TACTCTGGTT GTTGTGCCAA ATTGTGGTAC ACTTAGAAAA
3501 TTCTACAGTC GTCGATTTTT AGGGTGTCT CTTTCAACAC CTTTTTGTTA
3551 GTAATCATTG CCAGTAGTGC CTTTCATCAGT TAAGGGAGGT GTCCCAGCAC
3601 AGATCATTCT CAAAAGCGAG CAGGGAAGAG CTAGTGGGCA TGCTGAAGGC
3651 CAGCGTGGAC AGCAGGTGAG GCAGGTGCTC CTCACACCCA GACCTGGGCA
3701 TCTTCATTGA GGGAAAGAAA ACAGTCATTG TGCAAAATTC TGTTAGTCAG
3751 TGATTCTTTA CTGCAAAT CAGGGGCTTA GAAAATGAAA GCAAACACAA
3801 AACCTTGAGT GTGCTTTGGG AACCAAATGG ACCTTCTGGG ACAAGCTGAG
3851 CAAGCTGTAT GAACGCCACG TTTGTGAAGA GCTGAGGGTA TCAGGAGGGC
3901 CGACGCTGTG TTGGCATGCG CAGTAGGGGA TGAGGGTTAG CCATAGTATT
3951 CTTTGCAAAT GTGAAAGCGA GACATTATAT CTTCTCTTGC TTGGTGTAAC
4001 TAATCACTGT TAATTTTCAGG AAACAGAACT CATTAAAACT CCTTAGCAAA
4051 CCAGGTCTAC ATCCTGTTTT GTTTGCTGAG TGAGGTTAGT GGGAGTGGTC
4101 AAATTGGTAC TCTTGAGGA AGAAAACTG TCCTTCCTTC TCCAAAAAAG
4151 GAAAAATTAT AATAATATAA ATGACAAAAA TAAAAGAATT CTGTTTCCTG
4201 GAATAAGCAT TTCTTATTCC TAGTTGTAGG GACTCCTATT TTTACCTTCC
4251 GTTACAGTGT TGATTCATAA GAAATATTGT TACATTGAG ATAAC TTCAT
4301 CTGTATGGGG TATTTATTTG CAATGATGTC TGAGTACTGT ATTTTTTCTG
4351 TGCATTACCT TAGTGTGAGA ATGTTGGTCT TTATTTTAAA GTCATATGCA
4401 TGTTCCTCTG CCAAGGAACC TTTACACAGA CCCAAACAAA AAAATAATAA
4451 TCAAATGCCT TCAATTTCTG AGAAAATGAG GCAGAGCATG GAAAAGGAAT
4501 AGGAAGGAGA AATTAATTGA GATTTTCAGG ACACAGACAT ATGATGTGAA
4551 TGCCTACAAA GCCAGTGTGC ATAGGAACAG TGGGCCTGGG TAAAGAGTCA
4601 CATTGGTAGG

T03T90 10043360

1 MSAPSEEEY ARLVMEAQPE WLRAEVKRLS HELAETTREK IQAAEYGLAV
 51 LEEKHQKLQ FEELEVDYEA IRSEMEQLKE AFGQAHINHK KVAADGESRE
 101 ESLIQESASK EQYYVRKYLE LQTELKQLRN VLTNTQSENE RLSVAQELK
 151 EINQVEIQR GRLRDDIKEY KFREARLLQD YSELEENIS LQKQSVLRQ
 201 NQVEFEGCLKH EIKRLEETE YLNSQLEDAI RLKEISERQL EEALETIKTE
 251 REQNSLRKE LSHYMSTINDS FYTSHLHVS L DGLKFSDDAA EPNDAEALV
 301 NGFEHGGLAK LPLDNKTSTP KKEGLAPPSP SLVSDLLSEL NISEIQKLKQ
 351 QLMQMERKA GLLATLQDTQ KQLEHTRGSL SEQQEKVIRL TENLSALRRL
 401 QASKERQTAL DNEKDRDSHE DGYVEVDIN GPEILACKYH VAVAEAGELR
 451 BQLKALRSTH EAREAQAEE KGRYEAGQA LTEKVSLEK ASRQRELLA
 501 RLEKELKKVS DVAGETQGS L SVAQDELVT F SEELANLYHH VMCNNETRN
 551 RVMLDYVREG QGGAGRTSPG GRITSPEARGR RSPILLPKGL LAPEAGRADG
 601 GTGDSSPSFG SSLPSPLSDP RREPMNIYNL IAIIRDQIKH LQAAVDRITE
 651 LSRQRIASQE LGPAVDKKE ALMEEILKLK SLLSTKREQT TILRTVLKAN
 701 KQTAEVALAN LKSKYENKA MVTEIMMKLR NELKALKEDA ATFSSLRAMF
 751 ATRCDEYITQ LDEMQRQLAA AEDEKKTILNS LLRMAIQOKL ALTQRLELE
 801 LDHEQTRRGR AKAAPKTKPA TPSL*

FIGURE 2

1 ATGTGGGTGC TGGGCGAGTA CGAGCGACAC TGGGATTCCA TCAACTGGGA
 51 CTTTGGGAGC GAGTCCGGGG GTTGGCGGGA CTOGAGTCOG GGGCCTAGCG
 101 CCAGTCAGGG GCGCGGAGOC GCGCGCGGCG CCGCGGAGCA GGAGGAACTG
 151 CACTACATOC CCATCGCGGT CCTGGGCGGC GCGCGCTTOG GGGAGGCCAC
 201 GCTGTACCGC CGCACCGAGG ATGACTCACT GGTGTGTGTG AAGGAAGTGG
 251 AFTTGACCGC GCTGTCTGAG AAGGAACGTC GTGATGCGTT GAATGAGATT
 301 GTTATCTCTG CACTGCTGCA GCATGACAAC ATTATTGCGT ACTACAATCA
 351 CTTTCATGGAC AATACCAGCG TGCTGATTGA GCTGGAATAT TGTAATGGAG
 401 GGAACCTGTA TGACAAAATC CTTGGTCAGA AGGACAAGTT GTTTGAGGAA
 451 GAGATGGTGG TGTGGTACCT ATTTTCAGATT GTTTTCAGCAG TGAGCTGCAT
 501 CCATAAAGCT GGAATCCTTC ATAGAGATAT AAAGACATTA AATATTTTTC
 551 TGACCAAGGC AAACTGATA AACTTTGGAG ATTATGGCGT AGCAAAGGAA
 601 CTTAATTCTG AGTATTOCAT GGCTGAGAG CTTGTGGGAA CCGCATATTA
 651 CATGCTCTCA GAGCTCTGTC AAGGAGTAAA GTACAATTTC AAGTCTGATA
 701 TCTGGGCAGT TGGCTGGGTC ATTTTGTGAC TGCTTACCTT AAAGAGGAGG
 751 TTTGATGCTA CAAACCCACT TAACTGTGT GTGAAGATCG TGCAAGGAAT
 801 TCGGGCCATG GAAGTTGACT CTAGCCAGTA CTCTTTGGAA TTGATCCAAA
 851 TGGTTCATTC GTGCGTTGAC CAGGATCCTG AGCAGAGAC TACTGCAGAT
 901 GAATCTCTAG ATCGCCCTCT TCTCAGGAAA CGCAGGAGAG AGATGGAGGA
 951 AAAAGTCACT CTGCTTAATG CACTACAAA GAGACCAAGG TCAAGCACTG
 1001 TGAATGAGC ACCCATGCT GTAGTAACAT CACGAACCAG TGAAGTCTAT
 1051 GTTTGGGGTG GTGGAAAATC CACCCCCAG AACTGGATG TTATCAAGAG
 1101 TGGCTGTAGT GCGCGGAGG TCTGTGCAGG GAATACCCAC TTTGCTGTGG
 1151 TCACAGTGA GAAGGAACTG TACACTTGGG TGAACATCA AGGAGGCACT
 1201 AAATCCATG GTCAGCTGGG CCATGGAGAC AAAGCGCTCT ATGACAGGC

FIGURE 3

1251 AAAGCATGTG GAAAAGTTGC AAGGCAAAGC TATCCATCAG GTGTCATGTG
 1301 GTGATGATTT CACTGTCTGT GTGACTGATG AGGGTCAGCT CTATGCOCTC
 1351 GGATCAGATT ATTATGGCTG CATGGGGGTG GACAAAGTTG CTGGCOCTGA
 1401 AGTGCTAGAA CCCATGCAGC TGAACCTTCTT CCTCAGCAAT CCAGTGGAGC
 1451 AGGTCTCCTG TGGAGATAAT CATGTGGTGG TTCTGACAG AAACAAGGAA
 1501 GTCTATTCTT GGGGCTGTGG CGAATATGGA CGACTGGGTT TGGATTGAGA
 1551 AGAGGATTAT TATACACAC AAAAGGTGGA TGTTCCCAAG GCOCTTGATTA
 1601 TTGTTGCACT TCAATGTGGC TGTGATGGGA CATTTCGTGT GACCCAGTCA
 1651 GGCAAAGTGC TGGCCTGTGG ACTCAATGAA TTCAATAAGC TGGGTCTGAA
 1701 TCAGTGCATG TCGGGAATTG TCAACCATGA AGCATAOCAT GAAGTTCCCT
 1751 ACACAAAGTC CTTTACCTTG GCCAAACAGT TGTCCTTTTA TAAGATCCGT
 1801 ACCATTGCCC CAGGCAAGAC TCACACAGCT GCTATTGATG AGCGAGGCGG
 1851 GCTGCTGACC TTTGGCTGCA ACAAGTGTGG GCAGCTGGGC GTTGGGAACT
 1901 ACAAGAAGCG TCTGGGAATC AACCTGTTGG GGGGACCCCT TGGTGGGAAG
 1951 CAAGTGATCA GGGTCTCCTG CGGTGATGAG TTTCACCATG CTGCCACTGA
 2001 TGATAATCAC ATTTTGTGCT GGGGCAATGG TGGTAATGGC CGCCTGGCAA
 2051 TGACCCCCAC AGAGAGACCA CATGGCTCTG ATATCTGTAC CTCATGGCCT
 2101 CGGCTATTTT TTGGATCTCT GCATCATGTC CCGGACCTGT CTTGCGGTGG
 2151 ATGGCATAOC ATTCTCATOG TTGAGAAAGT ATTGAATTCT AAGACCATCC
 2201 GTTCCAATAG CAGTGGCTTA TOCATTGGAA CTGTGTTTCA GAGCTCTAGC
 2251 CCGGGAGGAG GCGGCGGGGG CGGGGGTGGT GAAGAAGAGG ACAGTCAGCA
 2301 GGAATCTGAA ACTOCTGACC CAAGTGGAGG CTTCOGAGGA ACAATGGAAG
 2351 CAGACCGAGG AATGGAAGGT TTAATCAGTC CCACAGAGGC CATGGGGAAC
 2401 AGTAAATGGG CCAGCAGCTC CTGTCTGGC TGGCTTGGAA AGGAGCTGGA
 2451 AAATGCAGAA TTTATCCCCA TGCTTGACAG CCCATCTCCT CTCAGTGCAG
 2501 CGTTTTGAGA ATCTGAGAAA GATACCCTGC CCTATGAGA GCTGCAAGGA

1251 1301 1351 1401 1451 1501 1551 1601 1651 1701 1751 1801 1851 1901 1951 2001 2051 2101 2151 2201 2251 2301 2351 2401 2451 2501

2551	CTCAAAGTGG	CCTCTGAAGC	TCCTTTGGAA	CACAAACCCC	AAGTAGAAGC
2601	CTCGTCACCT	CGGCTGAATC	CTGCAGTAAC	CTGTGCTGGG	AAGGGAACAC
2651	CAC TGACTCC	TCCTGGGTGT	GCGTGCAGCT	CTCTGCAGGT	GGAGGTTGAG
2701	AGATTGCAGG	GTCTGGTGT	AAAGTGTCCTG	GCTGAACAAC	AGAAGCTACA
2751	GCAAGAAAAC	CTCCAGATTT	TTACCCAACT	GCAGAAGTTG	AACAAGAAAT
2801	TAGAAGGAGG	GCAGCAGGTG	GGGATGCATT	CCAAAGGAAC	TCAGACAGCA
2851	AAGGAAGAGA	TGGAAATGGA	TOCAAAGCCT	GACTTAGATT	CAGATTCTCTG
2901	GTGCTCTCTG	GGAACAGACT	CCTGTAGACC	CAGCCTCTAG	

1 MSVLGEYERH CDSINSDFGS ESGGCGDSSP GPSASQGPRA GGGAAEQEEL
 51 HYIPIRVLGR GAFGEATLYR RTEDDSLVDVW KEVDLTRLSE KERRDALNEI
 101 VILALLQHDN IIAYYNHFMD NTLLIELEY CNGGNLYDKI LRQKDKLFEE
 151 EMVVWYLFQI VSAVSCIHA GILHRDIKTL NIFLTKANLI KLG DYGLAKK
 201 LNSEYSMAET LVGTPYYMSP ELCQGVKYNF KSDIWA VGC V IFELLTLKRT
 251 FDATNPLNLC VKIVQGIRAM EVDSSQYSLE LIQMVHSCLD QDPEQRPTAD
 301 ELLDRPLLRL RRREMEEKVT LLNAPTKRPR SSTVTEAPIA VVTSRTSEVY
 351 VWGGGKSTPQ KLDVIKSGCS ARQVCAGNTH FAVVTVEKEL YTWVNMQGGT
 401 KLHGQLGHGD KASYRQPKHV EKLQ GKAIHQ VSCGDDFTVC VTDEGQLYAF
 451 GSDYYGCMGV DKVAGPEVLE PMQLNFFLSN PVEQVSCGDN HVVVLTRNKE
 501 VYSWGCGEYG RLGLDSEEDY YTPQKVDVPK ALIIVAVQCG CDGTFLLTQS
 551 GKVLACGLNE FNKLGLNQCM SGIINHEAYH EVPYTTSFTL AKQLSFYKIR
 601 TIAPGKTHTA AIDERGRLLT FGCNKGQLG VGNYKKRLGI NLLGGPLGGK
 651 QVIRVSCGDE FTIAATDDNH IFAWNGGNG RLAMTPTERP HGSDICTSWP
 701 RPIFGSLHHV PDLSCRGWHT ILIVEKVLNS KTIRSNSSGL SIGTVFQSSS
 751 PGGGGGGGGG EEEDSQQESE TPDPSGGFRG TMEADRGMEG LISPTAMGN
 801 SNGASSCPG WLRKELENAE FIPMPDSPSP LSAAFSESEK DTLPEEELQG
 851 LKVASEAPLE HKPQVEASSP RLNPAVTCAG KGTPLTPPAC ACSSLQVEVE
 901 RLQGLVLKCL AEQQKLQQEN LQIFTQLQKL NKKLEGGQQV GMHSGKTQTA
 951 KEEMEMDPKP DLDSDSWCLL GTDSCRPSL*

FIGURE 4

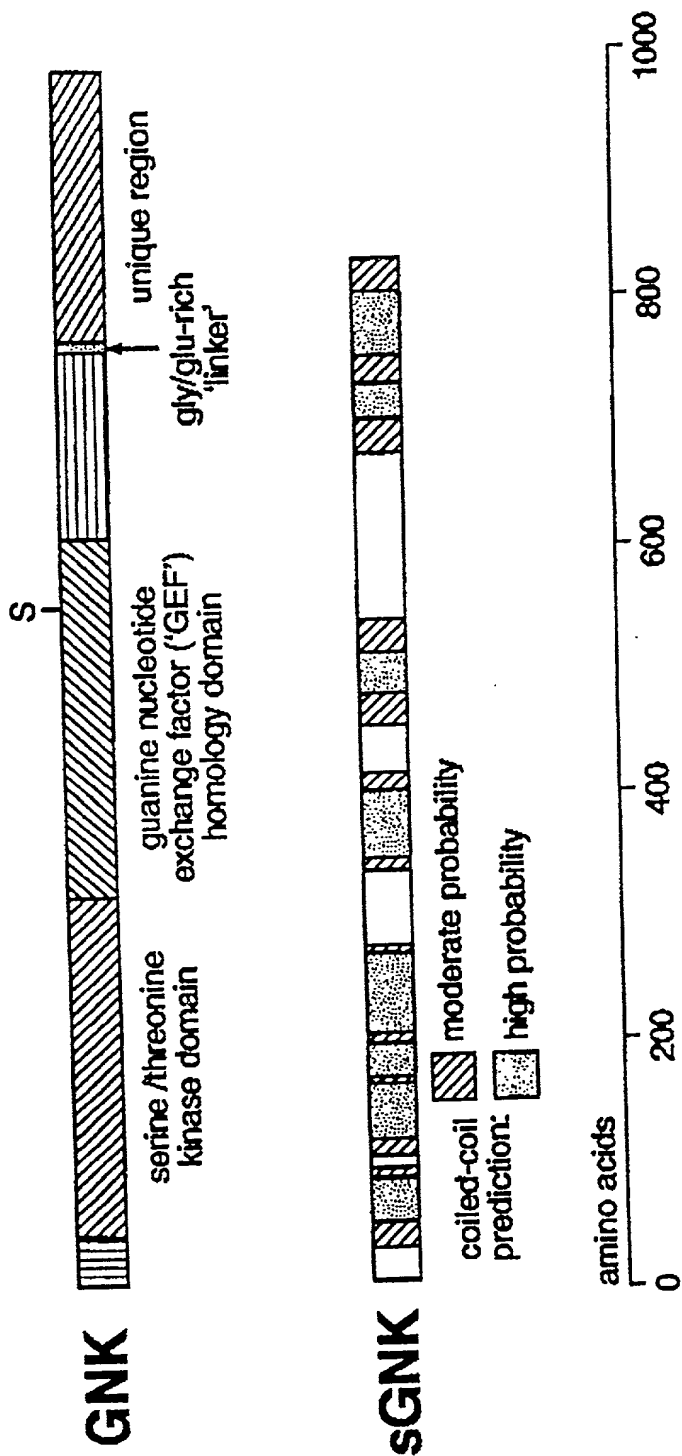


FIGURE 5

Putative GNK Domains and Structural Features

KINASE (44-315)

GUANINE NUCLEOTIDE EXCHANGE FACTOR (GEF) (318-605)

GLYCINE/ACIDIC-RICH TETHER (752-764)

C-TERMINAL DOMAIN WITH NO KNOWN HOMOLOGY OR FUNCTION (765-979)

1 MSVLGEYERH CDSINSDFGS ESGGCGDSSP GPSASQGPRA GGGAAEQEEL
 51 HYIPIRVLGR GAFGEATLYR RTEDDSLIVVW KEVDLTRLSE KERRDALNEI
 101 VILALLQHDN IIAAYNHFMD NTLLIELEY CNGGNLYDKI LRQKDKLFEE
 151 EMVVWYLFQI VSAVSCIHKA GILHRDIKTL NIFLTKANLI KLG DYGLAKK
 201 LNSEYSMAET LVGTPPYMSP ELCQGVKYNF KSDIWA VGC V IFELLTLKRT
 251 FDATNPLNLC VKIVQGIRAM EVDSSQYSLE LIQMVHSCLD QDPEQRPTAD
 301 ELLDRPLLRL RRREEMEEKVT LLNAPT KRPR SSTVTEAPIA VVTSRTSEVY
 351 VWGGGKSTPO KLDVIKSGCS ARQVCAGNTH FAVVTVEKEL YTWVNMQGGT
 401 KLHGQLGHGD KASYROPKHV EKLOGKAIHQ VSCGDDFTVC VTDEGOLYAF
 451 GSDYYGCMGV DKVAGPEVLE PMQLNFFLSN PVEQVSCGDN HVVVLTRNKE
 501 VYSWGCGEYG RLGLDSEEDY YTPQKVDVPK ALIIVAVQCG CDGTFLLTQS
 551 GKVLACGLNE FNKLGLNOCM SGIINHEAYH EVPYTTSFTL AKQLSFYKIR
 601 TIAPGKTHTA AIDERGRLLT FGCNKCGQLG VGN YKKRLGI NLLGGPLGGK
 651 QVIRVSCGDE FTIAATDDNH IFAWNGGNG RLA MTP TERP HGSDICTSWP
 701 RPIFGSLHHV PDLSCRGWHT ILIVEKVLNS KTIRSNSSGL SIGTVFQSSS
 751 PGGGGGGGGG EEEDSQESE TPDPSGGFRG TMEADRGMEG LISPTTEAMGN
 801 SNGASSSCPG WLRKELENAE FIPMPDSPSP LSAAFSESEK DTLPYEELQG
 851 LKVASEAPPLE HKPOVEASSP RLNP AVTCAG KGTPLTPPAC ACSSLOVEVE
 901 RLQGLVLKCL AEQOKLOEN LOIFTQLQKL NKKLEGGQOV GMHSGKTOTA
 951 KEEMEMDPKP DLSDSWCLL GTDSCRPSL

FIGURE 6

Bicaudal D -----MAAEVLQTVDPHY
 sGNK -----MSAPSEEEYARLVMEAPQEWL
 C-NAP1 (aa 121) NTHLEAQLQKAEAGAEQLADLRDIQEEKEEIQKKLSERHQEAAATQLEQLHQEAKRQ

Bicaudal D KTEIERLTKELTETTHEKIQAAEYGLVLEEKLTLKQQYDELEAEYDSLKQEELEQLKEAF
 sGNK RAEVKRLSHELAEATTREKIQAAEYGLAVLEEKHQLKQFEELEVDYEAIRSEMEQLKEAF
 C-NAP1 EEVLARAVQKEALVREKAALEVRLQAVEDRQDLAEQLQGLSSAKELLESSLFEAQQQN

Bicaudal D GQSFSIHRKVAEDGETREETLLQESASKEAYYL GKILEMQNELKQSRVVNTVQAEENRL
 sGNK GQAHTNHKKVAADGESREESLIQESASKEQYVVRKVLELQTELKQLRNVLNTQSENERL
 C-NAP1 SVIEVTKGQLEVQIQTVTQAKEVIQGEVRCLKLELDTERSQAE-QERDAAARQLAQAEQE

Bicaudal D TAVVQDLKENNEMVELQIRIMKDEIREYKFREARLLQDYTELEENITLQKLVSSTLKQNO
 sGNK ASVAQELKEINQVIEIQGRRLRDDIKEYKFREARLLQDYSELEENISLQKQVSVLRQNO
 C-NAP1 GKTALEQQKAAHEKEVNQLREKWE-KERSWHQQELAKALESLEREKMELEMLRLEKE-QTE

Bicaudal D VEVEGLKHEIKRFEETVLLNSQLEDAIRLKEIAEHQLEEALETLLKNEREQKNNLRKELS
 sGNK VEFEGLKHEIKRLEETEYLLNSQLEDAIRLKEISERQLEEALETLLKTEREQKNSLRKELS
 C-NAP1 MEAIQAQREEERTQAESALCQMLETEKERVSLLETLTQKELADASQQLERLRQMKV

Bicaudal D QYISLND----NHISISVDGLKFAEDGSEPNN--DDKMNGHIHGPLVKLNGDYRTPTLRK
 sGNK HYMSINDSFYTSHLHVSLLDGLKFSDDAAEPNNDAAELVNGFEHGLAKPLDNKTSPTPK
 C-NAP1 QKLKEQETTILQTLQEAQRELKEAARQHRDDLALQEESSLLQDKMDLQKQVEDLKS

Bicaudal D ----GESLNPVSDLFSELNISEIQKLKQQLMQVEREKAILLANLQESQTQLEHTKGALTE
 sGNK EGLAPPSPLVSDLLSELNISEIQKLKQQLMQMERKAGLLATLQDTQKQLEHTRGSLSE
 C-NAP1 QLVAQDDSDRLVEQEVQEKLRTEQYENRIQKELEREKASITLSLMEKEQRLLVLEADSI

Bicaudal D QHERVHRLTEHVNAMRGLQSSKELKAELDGEKGRDSGEEAHDYEVADINGLEILECKYRVA
 sGNK QQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDGDYEVADINGPEILACKYHVA
 C-NAP1 RQOELSALRQDMQEAQGEQKELSAQMELLRQEVKEK-EADFLAQEAQLLEELEASHITEQ

Bicaudal D VTEVIDLKAEIKALKEKYNKSVENYTDKAKYESKIOMYDEQVTSLEKTTKESGEKMAHM
 sGNK VAEAGELREQLKALRSTHEAREAQHAEEKGRYEAEGQALTEKVSLLEKASRQDRELLARL
 C-NAP1 QLRASLWAEAKAAQLQLRLRSTESQLEALAAEQPGNQAAQAAQLASLYSALQALGSV

Bicaudal D EKELQKMTSIANENHSTLNTAQDELVTTFSEELAQLYHHVCLCNNETPNRVMLDYYRQSRV
 sGNK EKELKVSDVAGETQGSLSVAQDELVTTFSEELANLYHHVCMCNNETPNRVMLDYYREG--
 C-NAP1 CESRPELSGGDSAPSVMGLEPDQNG--ARSLFKRGPLLTALSAEAVASALHKLHQDLWK

Bicaudal D TRSGSLKGPDDPRGLLSPRLARGVSSPVETRTSSEPVAKESTEPSKEPSPTKTPTTISP
 sGNK -QGG--AGRTSPGGRTSP--EARGRRSPILL-----PKGLLAPEAGRADGGTGDSSPSPG
 C-NAP1 TQQTRDVLRDQVQKLEERLTDTEAKSQVHTELQDLQRLSQNQEEKSKWEGKQNSLESE

Bicaudal D ITAPPSPVLDTSDIRKEPMNIYNLNAIIRDQIKHLQKAVDRSLQLSRQRAAARELAPMI
 sGNK SSLP--SPLSDP--RR-EPMNIYNLIAIIRDQIKHLQAAVDRTELSRQRIASQELGPAV
 C-NAP1 LMELHETMASLQSLRRAELQRMQAQGER----ELLQAAKENLTAQVEHLQAAVVEARAQ

Bicaudal D DKDKREALMEEILKLKSLSTKREQIATLRAVLKANKQTAEVALANLKNKYENKAMVTET
 sGNK DKDKREALMEEILKLKSLSTKREQITTLRTVLKANKQTAEVALANLKNKYENKAMVTET
 C-NAP1 ASAAGILEEDLRTARSALKLKNEEVESERERAQALQEQQELKVAQGKAIQEN-LALLTQT

Bicaudal D MTKLRNELKALKEDAATFSSLRMPATRCDEYVTQLDEMQRQLAAAEEDEKTLNLTLLRMA
 sGNK MMKLRLNELKALKEDAATFSSLRMPATRCDEYITQLDEMQRQLAAAEEDEKTLNLTLLRMA
 C-NAP1 LAEREEEVETLRGQIQELEKQREMOKAALELLSLDLKKRNQEVLDLQEQIQELEKCRSVL

Bicaudal D IQQKLALTQRLLEDLEFDHEQSRRSKGLG-KSKIGSPKV (-> 154 aa)
 sGNK IQQKLALTQRLLELDHEQTRRGRAKAAPKTKPATPSL*-----
 C-NAP1 EHLPMVQEREQKLTQVREQIRELEKDRETQRNVLEHQ (-> 914 aa)

Comparison of sGNK with coiled-coil domains of Human Bicaudal D
 and the human centrosomal NEK-1 substrate protein C-Nap1

FIGURE 7

sGNK is a substrate for GNK *in vitro*.

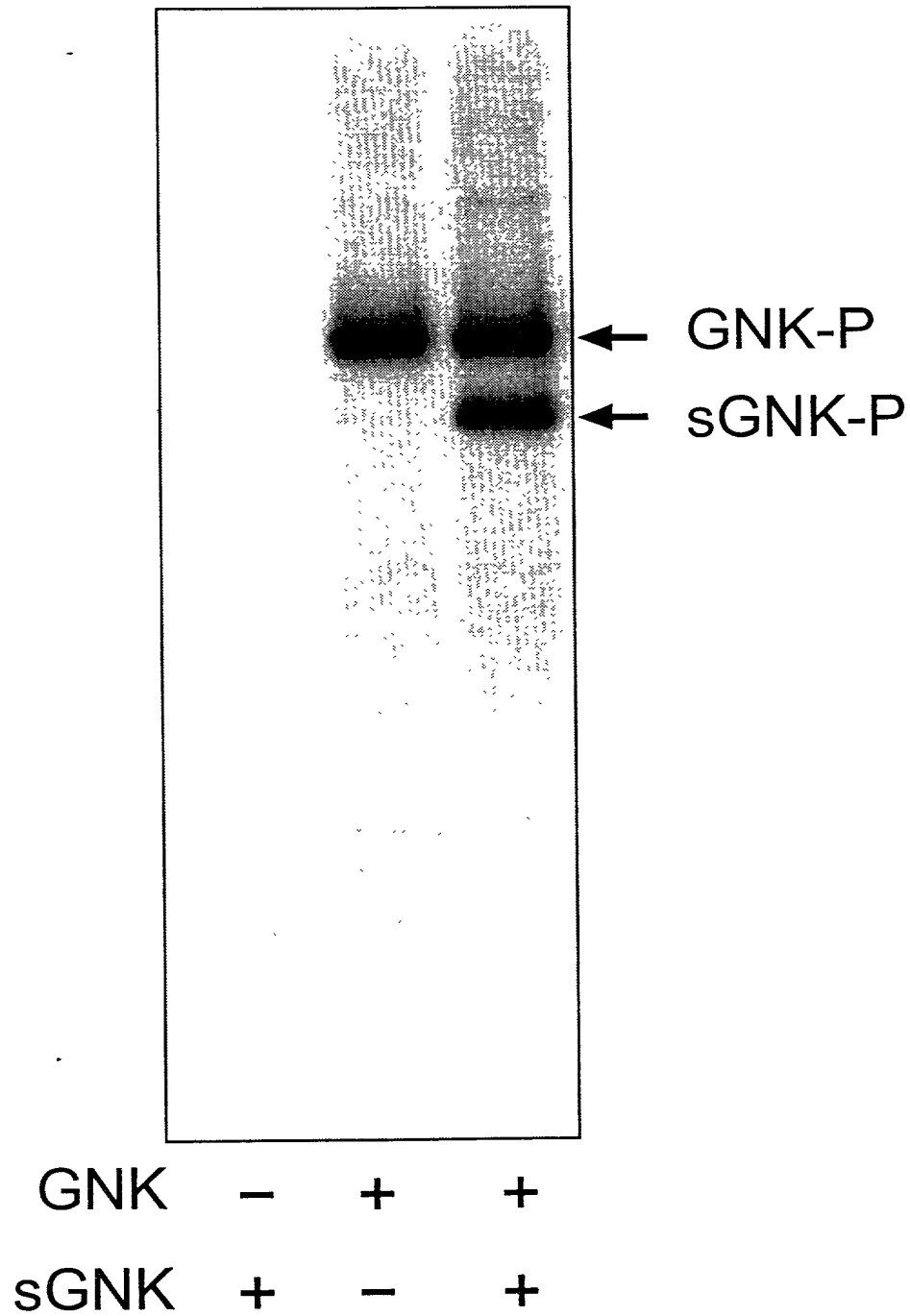


FIGURE 8

Final GNK purification step:
microbore Mono Q column chromatography

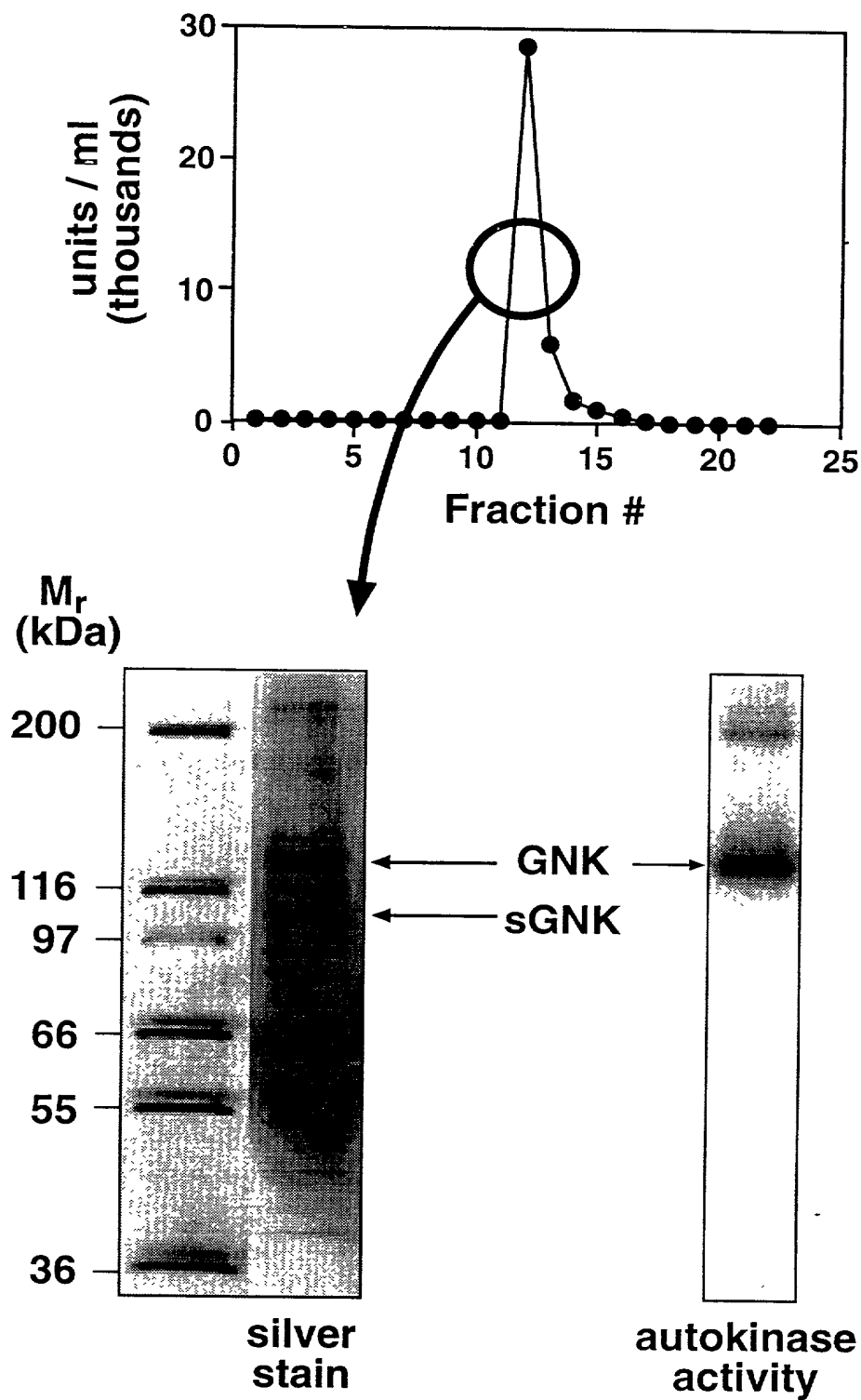


FIGURE 9



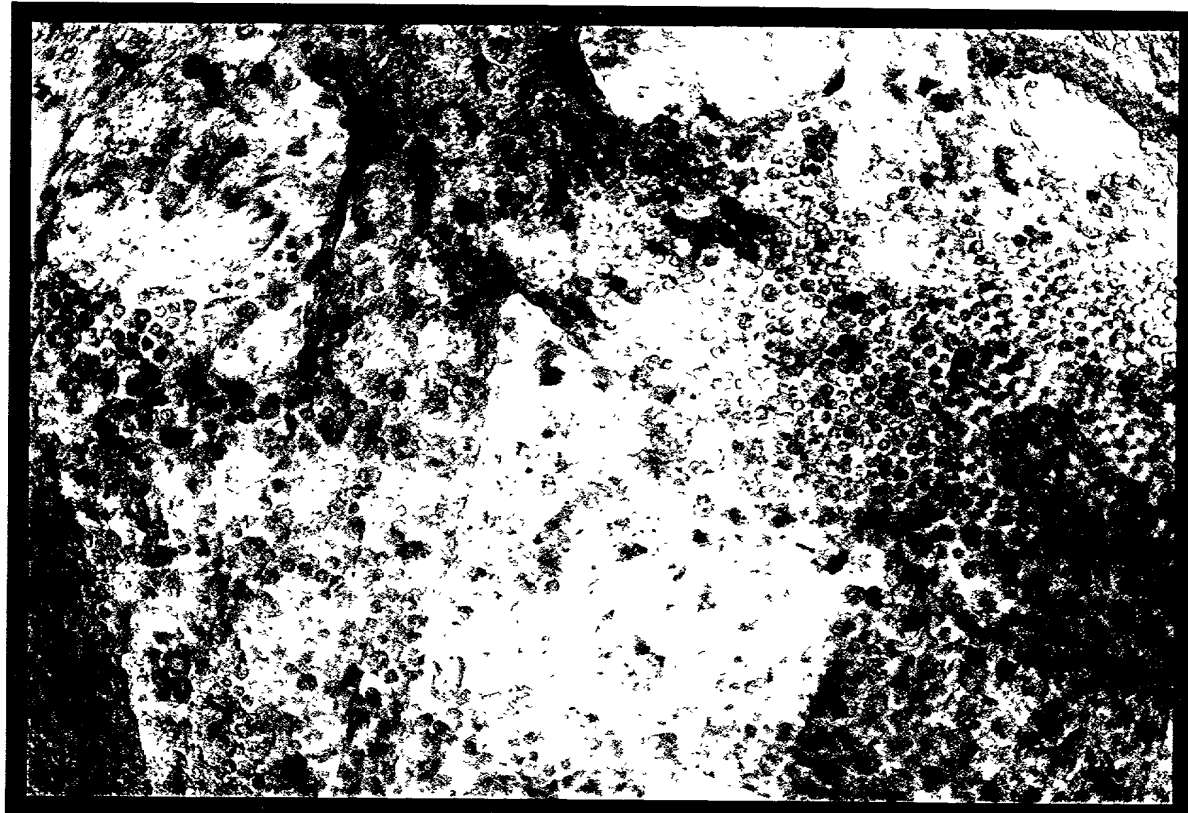


FIGURE 11A (top)
FIGURE 11B (bottom)